

# SEQUENCE LISTING

<110> Salter, Michael  
Gingrich, Jeffrey

<120> Method for Modification of NMDA Receptors Through Inhibition of Src

<130> 2560.004

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1

Lys Pro Ala Ser Ala Asp Gly His Arg  
1 5

<210> 2

<211> 20

<212> PRT

<213> Homo sapiens

<400> 2

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Lys Pro Ala Ser Ala  
1 5 10 15

Asp Gly His Arg  
20

<210> 3

<211> 4145

<212> DNA

<213> Homo sapiens

<400> 3

caaacaagtg cgccatttc accagcccag gctggcttct gctgttgact ggctgtggca	60
cctcaagcag cccctttccc ctctagcctc agtttatcac cgcaagagct accattcatc	120
tagcacaacc tgaccatcct cacactggtc agttccaacc ttcccaggaa tcttctgtgg	180
ccatgttcac tccggtttta cagaacagag aacagaagct cagagaagtg aagcaacttg	240
cccagctatg agagacagag ccaggatttg aaaccagatg aggacgctga ggcccagaga	300
gggaaagcca cttgcctagg gacacacagc ggggagaggt ggagcagggc ctctatttcg	360
agaccctga ctccacacct ggtgtttgtg ccaagacccc aggtgcctc ccaggtcctc	420
tgggacagcc cctgccttct accaggacca tgggtagcaa caagagcaag cccaaggatg	480
ccagccagcg gcgccgcagc ctggagcccg ccgagaacgt gcacggcgct ggcgggggcg	540
ctttccccgc ctcgcagacc cccagcaagc cagcctcggc cgacggccac cgcggcccca	600

gcgcggcctt	cgccccgcg	gccgccgagc	ccaagctgtt	cggaggcttc	aactcctcgg	660
acaccgtcac	ctccccgcag	agggcgggcc	cgctggccgg	tggagtgacc	acctttgtgg	720
ccctctatga	ctatgagtct	aggacggaga	cagacctgtc	cttcaagaaa	ggcgagcggc	780
tccagattgt	caacaacaca	gagggagact	ggtggctggc	ccactcgctc	agcacaggac	840
agacaggcta	catccccagc	aactacgtgg	cgccctccga	ctccatccag	gctgaggagt	900
ggtatttttg	caagatcacc	agacgggagt	cagagcgggt	actgctcaat	gcagagaacc	960
cgagagggac	cttcctcgtg	cgagaaagtg	agaccacgaa	aggtgcctac	tgcctctcag	1020
tgtctgactt	cgacaacgcc	aagggcctca	acgtgaagca	ctacaagatc	cgcaagctgg	1080
acagcggcgg	cttctacatc	acctcccgcg	cccagttcaa	cagcctgcag	cagctgggtg	1140
cctactactc	caaacacgcc	gatggcctgt	gccaccgcct	caccaccgtg	tgccccacgt	1200
ccaagccgca	gactcagggc	ctggccaagg	atgcctggga	gatccctcgg	gagtcgctgc	1260
ggctggagggt	caagctgggc	cagggctgct	ttggcgaggt	gtggatgggg	acctggaacg	1320
gtaccaccag	ggtggccatc	aaaaccctga	agcctggcac	gatgtctcca	gaggccttcc	1380
tgcaggaggc	ccaggtcatg	aagaagctga	ggcatgagaa	gctggtgcag	ttgtatgctg	1440
tggtttcaga	ggagcccatt	tacatcgta	cggagtacat	gagcaagggg	agtttgctgg	1500
actttctcaa	gggggagaca	ggcaagtacc	tgcggtgcc	tcagctggtg	gacatggctg	1560
ctcagatcgc	ctcaggcatg	gcgtacgtgg	agcggatgaa	ctacgtccac	cgggaccttc	1620
gtgcagccaa	catcctggtg	ggagagaacc	tgggtgtgaa	agtggccgac	tttgggctgg	1680
ctcggctcat	tgaagacaat	gagtacacgg	cgcggcaagg	tgccaaattc	cccatcaagt	1740
ggacggctcc	agaagctgcc	ctctatggcc	gcttcaccat	caagtcggac	gtgtggtcct	1800
tcgggatcct	gctgactgag	ctcaccacaa	agggacgggt	gccctaccct	gggatggtga	1860
accgcgaggt	gctggaccag	gtggagcggg	gctaccggat	gccctgcccg	ccggagtgtc	1920
ccgagtcctt	gcacgacctc	atgtgccagt	gctggcggaa	ggagcctgag	gagcggccca	1980
ccttcgagta	cctgcaggcc	ttcctggagg	actacttcac	gtccaccgag	ccccagtacc	2040
agccccggga	gaacctctag	gcacaggcgg	gcccagaccg	gcttctcggc	ttggatcctg	2100
ggctgggtgg	cccctgtctc	ggggcttgcc	ccactctgcc	tgctgtctgt	tggtcctctc	2160
tctgtggggc	tgaattgcca	ggggcgaggc	ccttcctctt	tggtagcatg	gaaggggctt	2220
ctggacctag	ggtggcctga	gagggcgggt	ggtatgcgag	accagcacgg	tgactctgtc	2280
cagctcccgc	tgtggccgca	cgcctctccc	tgcactccct	cctggagctc	tgtgggtctc	2340
tggaagagga	accaggagaa	gggctggggc	cggggctgag	ggtgcccttt	tccagcctca	2400
gcctactccg	ctcactgaac	tccttcccca	cttctgtgcc	acccccgggtc	tatgtcgaga	2460
gctggccaaa	gagcctttcc	aaagaggagc	gatgggcccc	tggccccgcc	tgctgtccac	2520

cctgccccctt gccatccatt ctggaacac ctgtaggcag aggctgccga gacagaccct	2580
ctgccgctgc ttccaggctg ggcagacaaa ggccttgccct ggcctgatga tgggtgggtgg	2640
gtgggatgag taccacctca aacctgccc tccttagacc tgagggacct ttcgagatca	2700
tcacttcctt gccccattt caccatggg gagacagttg agagcgggga tgtgacatgc	2760
ccaagggcac ggagcagttc agagtggagg cgggcttgga acccggtgct ccctctgtca	2820
tcctcaggaa ccaacaattc gtcggaggca tcatggaaag actgggacag cccaggaaac	2880
aaggggtctg aggatgcatt cgagatggca gattcccact gccgctgcc gctcagccca	2940
gctgttggga acagcatgga ggcagatgtg gggctgagct ggggaatcag ggtaaaaggt	3000
gcaggtgtgg agagagaggc ttcaatcggc ttgtgggtga tgtttgacct tcagagccag	3060
ccggctatga aaggagcga gccctcggc tctggaggca atcaagcaga catagaagag	3120
ccaagagtcc aggaggccct ggtcctggcc tccttccccg tactttgtcc cgtggcattt	3180
caattcctgg ccctgttctc ctcccaagt cggcaccctt taactcatga ggagggaana	3240
gagtgcctaa gcgggggtga aagaggacgt gttaccact gccatgcacc aggactggct	3300
gtgtaacctt ggggtggccc tgctgtctct ctgggctgca gagtctgcc cacatgtggc	3360
catggcctct gcaactgtc agctctggc caggccctgt ggcaggacac acatggtgag	3420
cctagccctg ggacatcagg agactgggt ctggctctgt tcggccttg ggtgtgtggt	3480
ggattctccc tgggcctcag tgtgccatc tgtaaagggg cagctgacag tttgtggcat	3540
cttgccaagg gtccctgtgt gtgtgtatgt gtgtgcatgt gtgcgtgtct ccatgtgcgt	3600
ccatatttaa catgtaaaaa tgtccccccc gctccgtccc ccaaacatgt tgtacatttc	3660
accatggccc cctcatcata gcaataacat tccactgcc aggggttctt gagccagcca	3720
ggccctgcca gtggggaagg aggccaagca gtgcctgcct atgaaatttc aacttttcct	3780
ttcatacgtc ttattatccc aagtcttctc ccgtccattc cagtcaaatc tgggctcact	3840
cacccagcg agctctcaa tccctctcca actgcctaag gccctttgtg taagggtgtct	3900
taatactgtc cttttttttt ttttaacagt gttttgtaga tttcagatga ctatgcagag	3960
gcctggggga cccctggctc tgggccgggc ctggggctcc gaaattcaa ggcccagact	4020
tgcggggggt ggggggggtat ccagaattgg ttgtaaatac tttgcatatt gtctgattaa	4080
acacaaacag acctcagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	4140
aaaaa	4145

<210> 4  
 <211> 535  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg Ser  
 1 5 10 15  
 Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe Pro  
 20 25 30  
 Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg Gly  
 35 40 45  
 Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe Gly  
 50 55 60  
 Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Pro  
 65 70 75 80  
 Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser  
 85 90 95  
 Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile  
 100 105 110  
 Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser Thr  
 115 120 125  
 Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser  
 130 135 140  
 Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser  
 145 150 155 160  
 Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu Val  
 165 170 175  
 Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp  
 180 185 190  
 Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys  
 195 200 205  
 Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn Ser  
 210 215 220  
 Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys  
 225 230 235 240  
 His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly  
 245 250 255

Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu  
 260 265 270  
 Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp  
 275 280 285  
 Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met  
 290 295 300  
 Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg  
 305 310 315 320  
 His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile  
 325 330 335  
 Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu  
 340 345 350  
 Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met  
 355 360 365  
 Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr  
 370 375 380  
 Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu  
 385 390 395 400  
 Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn  
 405 410 415  
 Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala  
 420 425 430  
 Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp  
 435 440 445  
 Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro  
 450 455 460  
 Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly  
 465 470 475 480  
 Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu  
 485 490 495  
 Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe Glu  
 500 505 510

Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln  
515 520 525

Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 5  
<211> 10  
<212> PRT  
<213> Artificial

<220>  
<223> src-activating peptide, used as a control

<220>  
<221> MOD\_RES  
<222> (4)..(4)  
<223> PHOSPHORYLATION

<400> 5

Glu Pro Gln Tyr Glu Glu Ile Pro Ile Ala  
1 5 10

<210> 6  
<211> 237  
<212> DNA  
<213> Homo sapiens

<400> 6  
tgactaacac ccttaattcc atccaccctc ctctccctag gaggcctgcc cccgctaacc 60  
ggcttttttgc ccaaattggac cattatcgaa gaattcacaa aaaacaatag cctcatcatc 120  
cccaccatca tagccaccat caccctcctt aacctctact tctacctacg cctaattctac 180  
tccacctcaa tcacactact ccccatatct aacaacgtaa aaataaaatg acagttt 237

<210> 7  
<211> 80  
<212> PRT  
<213> Homo sapiens

<400> 7

Trp Leu Thr Pro Leu Ile Pro Ser Thr Leu Leu Ser Leu Gly Gly Leu  
1 5 10 15

Pro Pro Leu Thr Gly Phe Leu Pro Lys Trp Thr Ile Ile Glu Glu Phe  
20 25 30

Thr Lys Asn Asn Ser Leu Ile Ile Pro Thr Ile Met Ala Thr Ile Thr  
35 40 45

Leu Leu Asn Leu Tyr Phe Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile  
6

50

55

60

Thr Leu Leu Pro Met Ser Asn Asn Val Lys Met Lys Trp Gln Phe Glu  
65 70 75 80

<210> 8  
<211> 1044  
<212> DNA  
<213> Homo sapiens

<400> 8  
attaatcccc tggcccaacc cgtcatctac tctaccatct ttgcaggcac actcatcaca 60  
gcgctaagct cgactgatt ttttacctga gtaggcctag aaataaacat gctagctttt 120  
attccagttc taaccaaaaa aataaacctt cgttccacag aagctgccat caagtatttc 180  
ctcacgcaag caaccgcata cataatcctt ctaatagcta tcctcttcaa caatatactc 240  
tccggacaat gaaccataac caatactacc aatcaatact catcattaat aatcataata 300  
gctatagcaa taaaactagg aatagcccc tttcacttct gagtcccaga gggtacccaa 360  
ggcacccttc tgacatccgg cctgcttctt ctcacatgac aaaaactagc ccccatctca 420  
atcatatacc aaatctctcc ctactaaac gtaagccttc tcctactct ctcaatctta 480  
tccatcatag caggcagttg aggtggatta aaccagacc agctacgcaa aatcttagca 540  
tactcctcaa ttaccacat aggatgaata atagcagttc taccgtacaa ccctaacata 600  
accattctta atttaactat ttatattatc ctaactacta ccgcattcct actactcaac 660  
ttaaactcca gcaccacgac cctactacta tctcgcacct gaaacaagct aacatgacta 720  
acacccttaa ttccatccac cctcctctcc ctaggaggcc tgcccccgct aaccgggcttt 780  
ttgccc aaat gggccattat cgaagaattc acaaaaaaca atagcctcat catccccacc 840  
atcatagcca ccatcaccct ccttaacctc tacttctacc tacgcctaata ctactccacc 900  
tcaatcacac tactcccat atctaacaac gtaaaaataa aatgacagtt tgaacataca 960  
aaaccacccc cattcctccc cacactcatc gcccttacca cgctactcct acctatctcc 1020  
ccttttatac taataatctt atag 1044

<210> 9  
<211> 347  
<212> PRT  
<213> Homo sapiens

<400> 9

Met Asn Pro Leu Ala Gln Pro Val Ile Tyr Ser Thr Ile Phe Ala Gly  
1 5 10 15

Thr Leu Ile Thr Ala Leu Ser Ser His Trp Phe Phe Thr Trp Val Gly  
20 25 30

Leu Glu Met Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys Lys Met  
 35 40 45  
 Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr Gln Ala  
 50 55 60  
 Thr Ala Ser Met Ile Leu Leu Met Ala Ile Leu Phe Asn Asn Met Leu  
 65 70 75 80  
 Ser Gly Gln Trp Thr Met Thr Asn Thr Thr Asn Gln Tyr Ser Ser Leu  
 85 90 95  
 Met Ile Met Met Ala Met Ala Met Lys Leu Gly Met Ala Pro Phe His  
 100 105 110  
 Phe Trp Val Pro Glu Val Thr Gln Gly Thr Pro Leu Thr Ser Gly Leu  
 115 120 125  
 Leu Leu Leu Thr Trp Gln Lys Leu Ala Pro Ile Ser Ile Met Tyr Gln  
 130 135 140  
 Ile Ser Pro Ser Leu Asn Val Ser Leu Leu Leu Thr Leu Ser Ile Leu  
 145 150 155 160  
 Ser Ile Met Ala Gly Ser Trp Gly Gly Leu Asn Gln Thr Gln Leu Arg  
 165 170 175  
 Lys Ile Leu Ala Tyr Ser Ser Ile Thr His Met Gly Trp Met Met Ala  
 180 185 190  
 Val Leu Pro Tyr Asn Pro Asn Met Thr Ile Leu Asn Leu Thr Ile Tyr  
 195 200 205  
 Ile Ile Leu Thr Thr Thr Ala Phe Leu Leu Leu Asn Leu Asn Ser Ser  
 210 215 220  
 Thr Thr Thr Leu Leu Leu Ser Arg Thr Trp Asn Lys Leu Thr Trp Leu  
 225 230 235 240  
 Thr Pro Leu Ile Pro Ser Thr Leu Leu Ser Leu Gly Gly Leu Pro Pro  
 245 250 255  
 Leu Thr Gly Phe Leu Pro Lys Trp Ala Ile Ile Glu Glu Phe Thr Lys  
 260 265 270  
 Asn Asn Ser Leu Ile Ile Pro Thr Ile Met Ala Thr Ile Thr Leu Leu  
 275 280 285



Asn Leu Tyr Phe Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile Thr Leu  
290 295 300

Leu Pro Met Ser Asn Asn Val Lys Met Lys Trp Gln Phe Glu His Thr  
305 310 315 320

Lys Pro Thr Pro Phe Leu Pro Thr Leu Ile Ala Leu Thr Thr Leu Leu  
325 330 335

Leu Pro Ile Ser Pro Phe Met Leu Met Ile Leu  
340 345

<210> 10  
<211> 150  
<212> DNA  
<213> Homo sapiens

<400> 10  
tgaataatag cagttctacc gtacaaccct aacataacca ttcttaattt aactatttat 60  
attatcctaa ctactaccgc attcctacta ctcaacttaa actccagcac cagcacccta 120  
ctactatctc gcacctgaaa caagctaaca 150

<210> 11  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 11

Trp Met Met Ala Val Leu Pro Tyr Asn Pro Asn Met Thr Ile Leu Asn  
1 5 10 15

Leu Thr Ile Tyr Ile Ile Leu Thr Thr Thr Ala Phe Leu Leu Leu Asn  
20 25 30

Leu Asn Ser Ser Thr Thr Thr Leu Leu Leu Ser Arg Thr Trp Asn Lys  
35 40 45

Leu Thr Trp  
50

<210> 12  
<211> 564  
<212> DNA  
<213> Homo sapiens

<400> 12  
attaatcccc tggcccaacc cgtcatctac tctaccatct ttgcaggcac actcatcaca 60  
gcgctaagct cgcactgatt ttttacctga gtaggcctag aaataaacat gctagctttt 120  
attccagttc taaccaaataa aataaacctt cgttccacag aagctgccat caagtatttc 180

ctcacgcaag caaccgcata cataatcctt ctaatagcta tcctcttcaa caatatactc 240  
 tccggacaat gaaccataac caatactacc aatcaatact catcattaat aatcataata 300  
 gctatagcaa taaaactagg aatagccccc ttctacttct gagtcccaga gggtacccaa 360  
 ggcacccctc tgacatccgg cctgcttctt ctcacatgac aaaaactagc ccccatctca 420  
 atcatatacc aaatctctcc ctactaaac gtaagccttc tcctcactct ctcaatctta 480  
 tccatcatag caggcagttg aggtggatta aaccagaccc agctacgcaa aatcttagca 540  
 tactcctcaa ttaccacat agga 564

<210> 13  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met Asn Pro Leu Ala Gln Pro Val Ile Tyr Ser Thr Ile Phe Ala Gly  
 1 5 10 15

Thr Leu Ile Thr Ala Leu Ser Ser His Trp Phe Phe Thr Trp Val Gly  
 20 25 30

Leu Glu Met Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys Lys Met  
 35 40 45

Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr Gln Ala  
 50 55 60

Thr Ala Ser Met Ile Leu Leu Met Ala Ile Leu Phe Asn Asn Met Leu  
 65 70 75 80

Ser Gly Gln Trp Thr Met Thr Asn Thr Thr Asn Gln Tyr Ser Ser Leu  
 85 90 95

Met Ile Met Met Ala Met Ala Met Lys Leu Gly Met Ala Pro Phe His  
 100 105 110

Phe Trp Val Pro Glu Val Thr Gln Gly Thr Pro Leu Thr Ser Gly Leu  
 115 120 125

Leu Leu Leu Thr Trp Gln Lys Leu Ala Pro Ile Ser Ile Met Tyr Gln  
 130 135 140

Ile Ser Pro Ser Leu Asn Val Ser Leu Leu Leu Thr Leu Ser Ile Leu  
 145 150 155 160

Ser Ile Met Ala Gly Ser Trp Gly Gly Leu Asn Gln Thr Gln Leu Arg  
 10

165

170

175

Lys Ile Leu Ala Tyr Ser Ser Ile Thr His Met Gly  
180 185